Patent claims

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the citA gene, chosen from the group consisting of

   a) polynucleotide which is identical to the extent of at least 70 % to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

   b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least to [sic] 70% to the amino acid sequence of SEQ ID No. 2,

   c) polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b),[sic] or c),

   the polypeptide preferably having the activity of the sensor kinase CitA.

2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.

3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

4. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

5. A DNA as claimed in claim 2 which is capable of replication, comprising

(i) the nucleotide sequence shown in SEQ ID no. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequences complementary to sequences (i) or (ii), and optionally

(iv) sense mutations of neutral function in (i).

6. A process as claimed in claim 5 [sic], w h e r e i n the hybridization is carried out under a stringency corresponding to at most 2x SSC.

7. A polynucleotide sequence as claimed in claim 2, which codes for a polypeptide which comprises the amino acid sequence shown in SEQ ID No. 2.

8. A vector pCR2.1citAint, which

8.1. carries an internal fragment of the citA gene 480 bp in size, shown in SEQ ID. No. 3,

8.2 the restriction map of which is reproduced in figure 1, and

8.3 which is deposited in the E. coli strain Top10/pCR2.1citAint at the Deutsche Sammlung für Mikroorganismen und Zellenkulturen [German Collection of Microorganisms and Cell Cultures] under no. DSM 13998 [sic]

9. An internal fragment of the citA gene with a length of 480 bp, shown in SEQ ID No. 3.

10. A coryneform bacterium, in which the citA gene is attenuated, preferably eliminated, in particular by deletion.

11. A process for the preparation of L-amino acids, in particular L-lysine,
w h e r e i n
it comprises carrying out the following steps,
a) fermentation of the coryneform bacteria which produced the desired L-amino acid and in which at least the citA gene is attenuated,
b) concentration of the desired product in the medium or in the cells of the bacteria and
c) isolation of the L-amino acid.

12. A process as claimed in claim 11,
w h e r e i n
bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

13. A process as claimed in claim 11,
w h e r e i n
bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

14. A process as claimed in claim 11,
w h e r e i n
expression of the polynucleotide(s) which codes (code) for the citA gene is reduced, in particular eliminated.

15. A process as claimed in claim 11,
w h e r e i n
the regulatory (or catalytic) properties of the polypeptide for which the polynucleotide citA codes are decreased.

16. A process as claimed in claim 11,
w h e r e i n
for the preparation of L-amino acids, in particular L-lysine, bacteria in which at the same time one or more of the genes chosen from the group consisting of

16.1 the dapA gene which codes for dihydrodipicolinate synthase,

16.2 the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase

16.3 the zwf gene which codes for glucose 6-phosphate dehydrogenase,

16.4 the pyc gene which codes for pyruvate carboxylase,

16.5 the lysE gene which codes for lysine export,

16.6 the lysC gene which codes for a feed back resistant aspartate kinase,

16.7 the zwa1 gene which codes for the Zwa1 protein

is or are enhanced, preferably over-expressed, are fermented.

17. A process as claimed in claim 11,
w h e r e i n
at the same time one or more of the genes chosen from the group consisting of:

17.1 the pck gene which codes for phosphoenol pyruvate carboxykinase,

17.2 the pgi gene which codes for glucose 6-phosphate isomerase,

17.3 the poxB gene which codes for pyruvate oxidase

17.4 the zwa2 gene which codes for the Zwa2 protein

is or are attenuated.

18. A process as claimed in one or more of the preceding claims, wherein microorganisms of the genus Corynebacterium glutamicum are employed.

19. A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes which code for sensor kinase CitA or have a high similarity with the sequence of the citA gene, wherein it comprises employing the polynucleotides comprising the sequences according to claims 1 to 4 as hybridization probes.